

## Appendix III: Alignment of intron A of M60321 with instant SEQ ID NO: 3

BLASTN 2.2.25+

Reference: Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000), "A greedy algorithm for aligning DNA sequences", J Comput Biol 2000; 7(1-2):203-14.

RID: N069FRCK111

Query= gi|330624|gb|M60321.1|HS5MIEP Human cytomegalovirus major immediate-early protein gene, 5' end

Length=2361

Sequences producing significant alignments:	Score (Bits)	E Value
lcl 35151 SID_3	630	0.0

## ALIGNMENTS

&gt;lcl|35151 SID\_3

Length=3584

Score = 630 bits (341), Expect = 0.0  
 Identities = 349/353 (99%), Gaps = 1/353 (0%)  
 Strand=Plus/Plus

Query	1737	TCGCTCGGCAGCTCCTTGCTCCTAACAGTGGAGGCCAGACTTAGGCACAGCACAAATGCC	1796
Sbjct	1010	TCGCTCGGCAGCTCCTTGCTCCTAACAGTGGAGGCCAGACTTAGGCACAGCACAAATGCC	1069
Query	1797	ACCACCACCAAGTGTGCCGCACAAGGCCGTGGCGGTAGGGTATGTGTCTGAAATGAGCTC	1856
Sbjct	1070	ACCACCACCAAGTGTGCCGCACAAGGCCGTGGCGGTAGGGTATGTGTCTGAAATGAGCTC	1129
Query	1857	GGAGATTGGGCTCGCACCG-TGACGCAGATGGAAGACTTAAGGCAGCGCAGAAGAAGAT	1915
Sbjct	1130	GGAGATTGGGCTCGCACCGCTGACGCAGATGGAAGACTTAAGGCAGCGCAGAAGAAGAT	1189
Query	1916	GCAGGCAGCTGAGTGTGTGTTCTGATAAGAGTCAGAGGTAACCTCCCGTTGCGGTGCTG	1975
Sbjct	1190	GCAGGCAGCTGAGTGTGTGTTCTGATAAGAGTCAGAGGTAACCTCCCGTTGCGGTGCTG	1249
Query	1976	TAAACGGTGGAGGGCAGTGTAGTCTGAGCAGTACTCGTTGCTGCCGCGCGCCACCAGA	2035
Sbjct	1250	TAAACGGTGGAGGGCAGTGTAGTCTGAGCAGTACTCGTTGCTGCCGCGCGCCACCAGA	1309
Query	2036	CATAATAGCTGACAGACTAACAGACTGTTCTCTTCCATGGGTCTTTTCTGTCAG	2088
Sbjct	1310	CATAATAGCTGACAGACTAACAGACTGTTCTCTTCCATGGGTCTTTTCTGTCAG	1362

Score = 449 bits (243), Expect = 1e-129  
 Identities = 248/250 (99%), Gaps = 1/250 (0%)  
 Strand=Plus/Plus

Query	1265	GTAAGTACCGCCTATAGACTCTATAGGCACACCCCTTTGGCTCTTATGCATGCTATACTG	1324
Sbjct	760	GTAAGTACCGCCTATAGACTCTATAGGCACACCCCTTTGGCTCTTATGCATGCTATACTG	819

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Query 1325 TTTTGGCTTGGGGCCTATACACCCCGCT-CCTTATGCTATAGGTGATGGTATAGCTTA 1383
          |||
Sbjct 820 TTTTGGCTTGGGGCCTATACACCCCGCTTCCTTATGCTATAGGTGATGGTATAGCTTA 879

Query 1384 GCCTATAGGTGTGGGTTATTGACCATTATTGACCACTCCCTATTGGTGACGATACTTTC 1443
          |||
Sbjct 880 GCCTATAGGTGTGGGTTATTGACCATTATTGACCACTCCCTATTGGTGACGATACTTTC 939

Query 1444 CATTACTAATCCATAACATGGCTCTTTGCCACAACATATCTCTATTGGCTATATGCCAATA 1503
          |||
Sbjct 940 CATTACTAATCCATAACATGGCTCTTTGCCACAACATATCTCTATTGGCTATATGCCAATA 999

Query 1504 CTCTGTCCTT 1513
          | |||||
Sbjct 1000 CACTGTCCTT 1009

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